

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2004, 09:22:37 ; Search time 2144.55 Seconds  
(without alignments)  
6739.548 Million cell updates/sec

Title: US-09-973-674A-16

Perfect score: 484

Sequence: 1 atcggaattggacacgggttt.....taaggcaacaaatgattga 484

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pin:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gsl1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	261.2	54.0	520	13	C14748
C 2	260.6	53.8	699	28	AQ990151
C 3	225.4	46.6	464	14	D80872
C 4	186.4	38.5	593	28	BZ351818
					C14748 C14748 Clon
					AQ990151 Rfc00873
					D80872 HUM13A12A
					BZ351818 hx72g05.g

5	184.4	38.1	654	28	BZ423610
6	138.4	28.6	1350	28	BZ567684
7	137	28.3	800	28	AQ991620
C 8	128	26.4	370	13	C15063
9	126.4	26.1	577	28	AQ242254
C 10	123	25.4	305	10	BF633873
C 11	123	25.4	305	10	BF633873
C 12	122.4	25.3	642	12	BF633873
13	121	25.0	773	13	BZ373430
C 14	120	24.8	834	28	BH396397
15	119	24.6	811	28	BZ577092
16	116.6	24.1	615	12	BF132679
17	116	24.0	527	9	AV394739
C 18	115	23.8	670	13	BQ796553
C 19	115	23.8	794	13	BQ800490
20	113.6	23.5	709	12	B1406315
C 21	112.6	23.3	695	9	AV783270
22	112	23.1	471	9	AV624871
23	112	23.1	489	9	AV620733
24	112	23.1	513	9	AV624394
25	111.2	23.0	581	28	BZ561122
C 26	111	22.9	560	9	AI670587
C 27	111	22.9	604	9	AI712133
28	110.4	22.8	812	14	CF668118
29	109.4	22.6	717	14	CF628504
30	108.6	22.4	523	13	BU765979
C 31	108.6	22.4	598	11	AY110686
32	108.6	22.4	770	14	CD574682
C 33	107.8	22.3	617	13	BU550772
C 34	107.2	22.1	693	14	CF475706
35	107	22.1	747	14	CF830014
36	107	22.1	765	14	CA783831
C 37	107	22.1	836	14	CF832762
C 38	107	22.1	843	14	CF832760
C 39	107	22.1	849	14	CF836632
40	105.4	21.8	615	14	CF811207
41	105.4	21.8	666	9	AV822490
42	105.4	21.8	732	12	BM658076
C 43	105	21.7	668	10	AW309700
44	104.6	21.6	661	12	BG129487
C 45	104.6	21.6	1106	14	CK215381

#### ALIGNMENTS

RESULT 1  
C14748/c  
LOCUS  
DEFINITION  
C14748 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens CDNA  
clone GEN-086802 3', mRNA sequence.  
ACCESSION  
C14748  
VERSION  
C14748.1 GI:1569455  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
C14748 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens CDNA  
clone GEN-086802 3', mRNA sequence.  
AUTHORS  
Fujiiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,  
Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,  
Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y.,  
Maekawa, H., Shin, S. and Nakamura, Y.  
Fujiiwara et al. (1995)  
Unpublished (1995)  
CONTACT  
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Otsuka GEN Research Institute  
Otsuka Pharmaceutical Co., Ltd  
463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan  
Tel: 0886-65-2888  
Fax: 0886-37-1035.  
LOCATION/Qualifiers  
1..520

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GEN-086802"
/clone_lib="Clontech human aorta polyA+ mRNA (#6572)"

ORIGIN
Query Match      54.0%; Score 261.2; DB 13; Length 520;
Best Local Similarity 93.9%; Pred. No. 4.7e-59;
Matches 295; Conservative 8; Mismatches 7; Indels 4; Gaps 3;

Qy 171 CGCAAGCTGTTCCCGGATACCGATCGGCGATTTAAAGGTGCCGATAGCCGCGAGCTGCT 230
Db 520 CGGAAGCTGTTCCCGGATACCGATCGGCGATTTAAAGGTGCCGATAGCCGCGAGCTGCT 230
Qy 231 ACAGGAGCTGTTCCCGGATACCGATCGGCGATTTAAAGGTGCCGATAGCCGCGAGCTGCT 290
Db 464 ACAGGAGCTGTTCCCGGATACCGATCGGCGATTTAAAGGTGCCGATAGCCGCGAGCTGCT 290
Qy 291 TATCATGCTCAGGACCGGATGTTCCCGGATTTAAAGGTGCCGATAGCCGCGAGCTGCT 350
Db 404 TATCATGCTCAGGACCGGATGTTCCCGGATTTAAAGGTGCCGATAGCCGCGAGCTGCT 350
Qy 351 CGAAGATCTCGGCTGCCGATGTTCCCGGATTTAAAGGTGCCGATAGCCGCGAGCTGCT 410
Db 285 CGAAGATCTCGGCTGCCGATGTTCCCGGATTTAAAGGTGCCGATAGCCGCGAGCTGCT 285
Qy 411 GGGATTTACCGGACCGGATGTTCCCGGATTTAAAGGTGCCGATAGCCGCGAGCTGCT 470
Db 284 GGGATTTACCGGACCGGATGTTCCCGGATTTAAAGGTGCCGATAGCCGCGAGCTGCT 284
Qy 471 AACAAATGATTGA 484
Db 224 AACAAATGATTGA 211

RESULT 2
AQ990151
LOCUS      699 bp      DNA      linear      GSS      14-AUG-2000
DEFINITION      Rf00873 Photorhabdus luminescens strain W14 M13 library
                  Photorhabdus luminescens genomic clone PLG00873, genomic survey
                  sequence.
ACCESSION      AQ990151.1      GI:9648745
VERSION      GSS.
KEYWORDS      Photorhabdus luminescens
SOURCE      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Photorhabdus.
ORGANISM      1 (bases 1 to 699)
            ffrrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
            Daborn,P.J., Bowen,D. and Blattner,F.R.
            A genomic sample sequence of the entomopathogenic bacterium
            Photorhabdus luminescens W14: potential implications for virulence
            Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
            MEDLINE      20378633
            PUBMED      10319786
COMMENT      Contact: ffrrench-Constant RH
            Department of Biology and Biochemistry
            University of Bath
            South Building, Bath BA2 7AY, UK
            Tel: (44) 1225 826621
            Fax: (44) 1225 826779
            Email: bsrscfbath.ac.uk
            This is one of 2,122 random reads from the M13 library. For
            annotation of identified clones (BLASTX, BLASTN and mapping to E.
            coli K12 genome) please see ffrrench-Constant et al. 2000, Nucleic
            Acids Res.
            Seq primer: M13 Forward
            Class: shotgun.
            Location/Qualifiers
            1..699
            /organism="Photorhabdus luminescens"

FEATURES
            source
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/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG00873"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
            library"
/note="Genomic DNA from strain W14 was size selected (1-2
            kb) and then cloned into M13 Janus."

ORIGIN
Query Match      53.8%; Score 260.6; DB 28; Length 699;
Best Local Similarity 73.3%; Pred. No. 7.6e-59;
Matches 346; Conservative 0; Mismatches 125; Indels 1; Gaps 1;

Qy 1 ATGCGATTGGACACGGTTCCTTACGATACATGCTTTCGCGTGAAGCCCAATATCATTT 60
Db 19 ATGAGGATCGGACACGGTTCCTTACGATACATGCTTTCGCGTGAAGCCCAATATATTC 78
Qy 61 GGTGCGGTACGCATTCCTTACGAAAGAGATTGCTGGCGCATTCCTGATGGCGACGTGGCG 120
Db 79 GGTGCGGTACGCATTCCTTACGAAAGAGATTGCTGGCGCATTCCTGATGGGTGATGTTGCT 138
Qy 121 CTCATGCGTTGACCGATGCTTTCGCGCGCGCGCGCTGGGGGATATCGGCAAGCTG 180
Db 139 CTCATGCGCGCGCGCGCGCTTTCGCGCGCGCGCTGGGGGATATCGGCAAGCTG 198
Qy 181 TTCCCGGATACCGATTCGCGCATTTAAAGGTGCCGATAGCCGCGAGCTGCTACGCGAAGCC 240
Db 199 TTCCCGGATACCGATTCGCGCGCGCTTTCGCGCGCGCGCTGGGGGATATCGGCAAGCC 258
Qy 241 TGGCGTTCGTTTACGCGCGCGCGCTTTCGCGCGCGCGCTGCTACGCGAAGCTGCT 300
Db 259 TATTCACGATACGAGAAAGGGTTATCGGATTCGCGATTCGATATTCGATATTCGCT 318
Qy 301 CAGGACCGAAGATGTTGCCGCGCATTCGCGCGCGCGCTGTTTATTCGCGCGAGCTC 360
Db 319 CAGGACCGAAGATGTTGCCGCGCATTCGCGCGCGCGCTGTTTATTCGCGCGAGCTC 378
Qy 361 GGCTGCCATATGCGATGTTTAAAGGTGCCGCGCGCGCTGTTTATTCGCGCGAGCTC 419
Db 379 CAATGCCACATGATGATCAATCAATGTTAAAGCGCGCGCTGTTTATTCGCGCGAGCTC 438
Qy 420 CGGACGTGGGGAAGGATTCGCTGCGAAGCGCGCGCTGCTATCATTAAGGCA 471
Db 439 GGGCGGTAAGAAAGTATTCGCTGCGAAGCGCGCGCTGCTTTCGCTGTTAAGGAA 490

RESULT 3
D80872/c
LOCUS      464 bp      mRNA      linear      EST      09-FEB-1996
DEFINITION      HUM113A12A Human fetal brain (TFujiwara) Homo sapiens cDNA clone
                  GEN-113A12 3', mRNA sequence.
ACCESSION      D80872.1      GI:1178749
VERSION      EST.
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 464)
            Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M.,
            Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H.,
            Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y.,
            Maekawa,H., Shin,S. and Nakamura,Y.
            Fujiwara et al. (1995)
            Unpublished (1995)
            Contact: Teitomu Fujiwara
            Otsuka GEN Research Institute
            Otsuka Pharmaceutical CO., Ltd
            463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
            Tel: 0886-65-2888
            Fax: 0886-37-1035.

TITLE      Fujiwara et al. (1995)
JOURNAL
COMMENT
```

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FEATURES
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      1..464
        /organism="Homo sapiens"
        /mol_type="rRNA"
        /db_xref="taxon:9606"
        /clone="GEN-113A12"
        /dev_stage="fetal"
        /clone_lib="Human fetal brain (TFujiwara)"
        /note="Organ: brain"

ORIGIN
  Query Match      46.6%; Score 225.4; DB 14; Length 464;
  Best Local Similarity 97.2%; Pred. No. 1.7e-49;
  Matches 246; Conservative 4; Mismatches 1; Indels 2; Gaps 2;

QY 233 GCGAAGCCTGCGCGTATTTCAGGCGAAGGGTTATACCCCTGGCGAAGCTGCGATGCACTA 292
Db 464 SCGAAGCCTGCGCGTATTTCAGGCGAAGGGTTATACCCCTGGCGAAGCTGCGATGCACTA 405

QY 293 TCATCGCTCAGGCGACCGAAGATGTTGCCGCA-CATTCCACAAATGCGCGTGTATTATGCC 351
Db 404 TCATCGCTCA-GCAGCGAAGATGTTGCCGATCATTCACAAATGCGCGTGTATTATGCC 346

QY 352 GAAGATCTGCGCTGCATATGATGATGTTAACTGAAAGCCACTACTACGAAAAAATG 411
Db 345 GAAGATC GCGCTGCATATGATGATGTTAACTGAAAGCCACTACTACGAAAAAATG 286

QY 412 GGATTTACCGACGTGGGGAAGGATTCCTGTGAAGCGTGGCGCTACTACTTAAGGCA 471
Db 285 GGATTTACCGACGTGGGGAAGGATTCCTGTGAAGCGTGGCGCTACTACTTAAGGCA 226

QY 472 ACAAATGATTGA 484
Db 225 ACAAATGATTGA 213

RESULT 4
BZ351818/c
LOCUS
DEFINITION
  BZ351818 593 bp DNA linear GSS 12-NOV-2002
  hx72g95.g1 WGS-SbicolorF (JM107 adapted methyl filtered) Sorghum
  bicolor genomic clone hx72g95 5', genomic survey sequence.
ACCESSION
  BZ351818
VERSION
  BZ351818.1 GI:24915450
KEYWORDS
  GSS.
SOURCE
  Sorghum bicolor (sorghum)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
    clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
  1 (bases 1 to 593)
    Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N.,
    Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
    Zutavern,I., Palmer,L., McCombie,W.R. and Martienssen,R.A.
    Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)
    Unpublished (2002)
  Contact: W. Richard McCombie
  Lita Annenberg Hazen Genome Sequencing Center
  Cold Spring Harbor Laboratory
  PO Box 100, Cold Spring Harbor, NY 11724, USA
  Tel: 516 367 8884
  Fax: 516 367 8874
  Email: mcombie@cshl.org
  Plate: bx72 row: g column: 05
  Seq primer: -21M13UnivRev
  Class: shotgun
  High quality sequence stop: 593.
  Location/Qualifiers
    1..593
      /organism="Sorghum bicolor"
      /mol_type="genomic DNA"
      /db_xref="taxon:4558"
      /clone="hx72g95"
      /lab_host="JM107 or DH5a"

FEATURES
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    Location/Qualifiers
      1..654
        /organism="Sorghum bicolor"
        /mol_type="genomic DNA"
        /db_xref="taxon:4558"
        /clone="id51c09"
        /lab_host="DH5a"

/clone_lib="WGS-SbicolorF (JM107 adapted methyl filtered)"
/note="Site 1: Xba I; Site 2: Xba I; The vector was
digested with XbaI and one nucleotide was added by fill in
in the recessive 3' end. The genomic DNA was nebulized,
end repaired, adaptor ligated and size fractionated using
sephadex. The resulting fragments were between 0.8 and 3
kb and were cloned into the vector (.x/y reads in M13mp19,
.b/g reads in pUC19). The same ligation was transformed in
either JM107 or DH5a."

ORIGIN
  Query Match      38.5%; Score 186.4; DB 28; Length 593;
  Best Local Similarity 78.5%; Pred. No. 4.9e-39;
  Matches 223; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 ATGCGAATGGACACGGTTTTGACGTACATCGCTTTGGCGGTGAAGGCCCAATTATCAT 60
Db 289 ATGCGTATCGGTACCGGTTTTGACGTGACCGGTTTGGCGGAGGCCCGCTGCTGATT 230

QY 61 GGTGGCGTACGATCTCTTACGAAAAGGATGCTGGCGCATTTGATGGCGACGCTGGCG 120
Db 229 GCGCGGTTGCGTATTTCCCTTCGAAACAGGCTTTTATTTGGCATTTCCGACGGCATGTGCG 170

QY 121 CTCATGCTGTGACCGATGCTTCTTGGCGCGCGCTGGGGGATATCGGAAGCTG 180
Db 169 CTGATGCGCTGACCGACGCGCTGCTGGCGCGGTGGCGGACATCGGAAAATG 110

QY 181 TTCCCGGATACCGATCGCGCATTTAAAGGTCCGATACCGCGAGCTCTACCGGAAGCC 240
Db 109 TTCCCGGACCCGATCGCGCATTCAAAGGCGCGACACCGCGGTTTCTGGGGAAACC 50

QY 241 TGGCGTGTATTACAGCGAAGGGTTATACCTTGGCAACGTCGA 284
Db 49 TGGCGTGTATCCAGCGAGGGCTTCGCGATTGCGCAACGTTGA 6

RESULT 5
BZ423610
LOCUS
DEFINITION
  BZ423610 654 bp DNA linear GSS 10-DEC-2002
  id51c09.g1 WGS-SbicolorF (DH5a methyl filtered) Sorghum bicolor
  genomic clone id51c09 5', genomic survey sequence.
ACCESSION
  BZ423610
VERSION
  BZ423610.1 GI:26373013
KEYWORDS
  GSS.
SOURCE
  Sorghum bicolor (sorghum)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
    clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
  1 (bases 1 to 654)
    Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N.,
    Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
    Zutavern,T., Palmer,L., McCombie,W.R. and Martienssen,R.A.
    Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)
    Unpublished (2002)
  Contact: W. Richard McCombie
  Lita Annenberg Hazen Genome Sequencing Center
  Cold Spring Harbor Laboratory
  PO Box 100, Cold Spring Harbor, NY 11724, USA
  Tel: 516 367 8884
  Fax: 516 367 8874
  Email: mcombie@cshl.org
  Plate: id51 row: c column: 09
  Seq primer: -21M13UnivRev
  Class: shotgun
  High quality sequence stop: 654.
  Location/Qualifiers
    1..654
      /organism="Sorghum bicolor"
      /mol_type="genomic DNA"
      /db_xref="taxon:4558"
      /clone="id51c09"
      /lab_host="DH5a"

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/clone lib="WGS-SbicolorF (DH5a methyl filtered)"  
 /note="Site 1: Xba I; Site 2: Xba I; The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, b/g reads in pUC19). The same ligation was transformed into DH5a."

## ORIGIN

Query Match 38.1%; Score 184.4; DB 28; Length 654;  
 Best Local Similarity 80.8%; Pred. No. 1.8e-38;  
 Matches 215; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 ATGCGAATTGACACGGTTTTCAGCTATGCTTTGGCGGTGAAGGCCCAATTATCATTT 60  
 Db ATGGGTATCGGTACCGTTTTCAGCTATGCTTTGGCGGTGAAGGCCCGCTGCTGATT 441

QY 61 GGTGGCGTACGATTCCTTACGAAAGGATTGCTGGCGCATTCCTGATGGCGACGCTGGCG 120  
 Db GCGCGGTGCGGATTCCTTACGAAAGGATTGCTGGCGCATTCCTGATGGCGACGCTGGCG 501

QY 121 CTCATGCTGTTGACGATGCTATGCTTTGGCGGCGGCTGGCGGATATCGGCAAGCTG 180  
 Db CTGATGCTGACGCGCTGCTGGCGGCGGCTGGCGGATATCGGCAAGCTG 561

QY 181 TTCGCGGATACGATTCGCGCATTTAAAGTGGCGATAGCGCGAGCTGCTAGCGAAGCC 240  
 Db TTCGCGGATACGATTCGCGCATTTAAAGTGGCGATAGCGCGAGCTGCTAGCGAAGCC 621

QY 241 TGGCGTCTGATTCAGCGCAAGGGTTA 266  
 Db TGGCGTCTGATTCAGCGCAAGGGGCTA 647

## RESULT 6

BZ567684  
 LOCUS pacs2-164\_7159.xl pacs2-164 Pseudomonas aeruginosa genomic clone  
 DEFINITION pacs2-164\_7159, genomic survey sequence.

ACCESSION BZ567684  
 VERSION BZ567684.1 GI:27199364

KEYWORDS  
 SOURCE Pseudomonas aeruginosa  
 ORGANISM Pseudomonas aeruginosa  
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

REFERENCE  
 1 (bases 1 to 1350)  
 Burns, J.L., Kaul, R. and Olsen, M.V.  
 Whole-Genome-Sequence variation among multiple isolates of Pseudomonas aeruginosa library  
 J. Bacteriol. (2002) In press

JOURNAL  
 COMMENT Contact: Chris K. Raymond  
 Genome Center  
 University of Washington  
 Box 352145, Seattle, WA 98105-2145, USA  
 Tel: 2062216954  
 Fax: 2066857244  
 Email: craymond@u.washington.edu  
 Class: shotgun.

## FEATURES

source  
 1. .1350  
 /organism="Pseudomonas aeruginosa"  
 /mol\_type="genomic DNA"  
 /strain="2-164"  
 /db\_xref="taxon:287"  
 /clone="pacs2-164\_7159"  
 /clone\_lib="pacs2-164"  
 /note="clinical isolate 2-164 Whole genomic shotgun library."

## ORIGIN

Query Match 28.6%; Score 138.4; DB 28; Length 1350;  
 Best Local Similarity 58.0%; Pred. No. 4.7e-26;  
 Matches 244; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 1 ATGCGAATTGACACGGTTTTCAGCTATGCTTTGGCGGTGAAGGCCCAATTATCATTT 60  
 Db ATGCAACTCGGCGCATGGTTTACACGTGATCGCTTCGGCGAGGGCGACTTGATCACCCCTC 233

QY 61 GGTGGCGTACGATTCCTTACGAAAGGATTGCTGGCGCATTCCTGATGGCGACGCTGGCG 120  
 Db GCGCGAGTGGCGATTCGCCAACAATGCGTGGTGGCGCATTCCTGATGGCGACGCTGGCG 293

QY 121 CTCATGCTGTTGACGATGCTATGCTTTGGCGGCGGCGCTGGCGGATATCGGCAAGCTG 180  
 Db CTGACAGCTTGTTCGATGCGCTCTCGCGCGGCATCTCTCGCGGACATCTTCTTAGCAC 353

QY 181 TTCGCGGATACGATTCGCGCATTTAAAGTGGCGATAGCGCGAGCTGCTAGCGAAGCC 240  
 Db TCTCGGCACACCGACCGCTGGTTCAAGGGCTCTTACGTGCGCGCTGGTGGCGACGCTG 413

QY 241 TGGCGTCTGATTCAGCGCAAGGGTTTATACCTTTGGCAACGTGCTGATCATCATGCT 300  
 Db ATGCGCATGCTGGCGAGCTGGCTGAAAGTTGGCAACGTGCTGCGCACCATTTGCGTCT 473

QY 301 CAGGCACCGAAGATCTTGC CGCACATTCACAAATCGCGGTGTTTATTTGCCGAAATCTC 360  
 Db CATGCGCGAAGATGGCTCGGCATCGAGACCATGAGCGGTTGATCGCCAAAGGACCAT 533

QY 361 GCGTCCCATATGATGATGTTTAACTGAAAGCCACTACTACGGAATACTGGGATTTACC 420  
 Db TGCCTTTTGGCATGAGCTGAACGTCTTGGCCCACTTCTCGAGAGCTTGTATTAACC 593

QY 421 G 421  
 Db 594 G 594

## RESULT 7

AQ991620  
 LOCUS Rf01133F Photorhabdus luminescens strain W14 M13 library  
 DEFINITION Photorhabdus luminescens genomic clone PLG01133F, genomic survey sequence.

ACCESSION AQ991620  
 VERSION AQ991620.1 GI:9650289

KEYWORDS  
 SOURCE Photorhabdus luminescens  
 ORGANISM Photorhabdus luminescens  
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.

REFERENCE  
 1 (bases 1 to 800)  
 ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.  
 A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence

JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

Contact: ffrench-Constant RH  
 Department of Biology and Biochemistry  
 University of Bath  
 South Building, Bath BA2 7AY, UK  
 Tel: (44) 1225 826621  
 Fax: (44) 1225 826779  
 Email: bsr@bath.ac.uk  
 This is one of a selected subset of flipped clones from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.  
 Seq primer: M13 Reverse  
 Class: shotgun.  
 Location/Qualifiers

## FEATURES

```

source
1. .800
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG01133F"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13 library"
/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN
Query Match
Best Local Similarity 28.3%; Score 137; DB 28; Length 800;
Matches 182; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 214 GATAGCGGAGCTGCTAGCGAAGCTGGCGTGGTATTCAGCGAAGGTTATACCTT 273
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 30 GATAGCGGTAATATTGGCGAAGCTATTACGCTATCANAGAAAGGTTATCGATT 89
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 274 GGCACGTCGATGCTCACTATCATCTCAGGACCGAAGATGTCGCGACATTCACAA 333
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 90 GCAATCTGGATATTACGATATTCGCTCAAGCACCCAAATGCTCGCATATTCACAA 149
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 334 ATGCGCGTGTATTGCGGAGATCTGGCTGCCATATGGATGATGTTAACTGAAAGCC 393
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 150 ATGAGAGTCAATCTGGCAGAGATCTCAATGCCACATTAATGTTAAAGCC 209
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 394 ACTACTACGGAATACTGGGATTTACCGAGTGGGAGGAGGATTCCTGTGAAGCGGTG 453
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 210 ACACTACGGAATAATAGGATTTGTTGGCGTAAAGAGGTATTGCTTGGAGCACTT 269
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 454 GCGCTACTCATTAAAGCA 471
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 270 GCTTGTGCTGTTAAGGAA 287
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
C15063/c
LOCUS
DEFINITION
C15063 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA
clone GEN-113F02 3', mRNA sequence.
ACCESSION
C15063
VERSION
C15063.1 GI:1569770
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 370)
Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,
Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,
Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y.,
Maekawa, H., Shin, S. and Nakamura, Y.
Fujiwara et al. (1995)
Unpublished (1995)
CONTACT: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.

FEATURES
source
1. 370
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GEN-113F02"
/clone_lib="Clontech human aorta polyA+ mRNA (#6572)"

ORIGIN
Query Match
26.4%; Score 128; DB 13; Length 370;

```

```

Best Local Similarity 95.6%; Pred. No. 1.7e-23;
Matches 151; Conservative 2; Mismatches 3; Indels 3; Gaps 2;

QY 327 TCACAAATGCGCGTGTATTATTCGCGAAGATCTCGGCTGCCATATGGATGATGTTAACCT 386
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 368 TCACAAATGCGCGTGTATTATTCGCGAAGATCTCGGCTGCCATATGGATGATGTTAACCT 309
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 387 GAAAGCCACTACTACGGAATACTGGGATTTACCGAGCTGGGAGGAGGATTCCTGTGA 446
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 308 GAAAGCCACTACTACGGAATACTGGGATTTACCGAGCTGGGAGGAGGATTCCTGTGA 252
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 447 AGCGTGGCGTACTCATTAAAGCAACAAATGATTGA 484
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 251 AGCGTGGCGTACTCATTAAAGCAACAAATGATTGA 214
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
AQ242254
LOCUS
DEFINITION
3P02-39r Ochrobactrum anthropi BAC Library Ochrobactrum anthropi
genomic clone 3P02-39r, genomic survey sequence.
ACCESSION
AQ242254
VERSION
AQ242254.1 GI:3688053
KEYWORDS
GSS.
SOURCE
Ochrobactrum anthropi
ORGANISM
Ochrobactrum anthropi
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Ochrobactrum.
REFERENCE
1 (bases 1 to 577)
Tomkins, J., Miller-Smith, H., Sasinowski, M., Choi, W., Sasinowska, H.,
Verce, M., Freedman, D., Dean, R. and Wing, R.A.
Physical map and gene survey of the Ochrobactrum anthropi genome
using bacterial artificial chromosome contigs
Microb. Comp. Genomics 4 (3), 203-217 (1999)
20055259
10587947
PUBMED
COMMENT
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Class: BAC ends
High quality sequence stop: 1.
Location/Qualifiers
1. 577
/organism="Ochrobactrum anthropi"
/mol_type="genomic DNA"
/db_xref="taxon:529"
/clone="3P02-39r"
/lab_host="DH10B E. coli"
/clone_lib="Ochrobactrum anthropi BAC Library"
/note="Vector: pBelosAC11; Site: 1: HindIII; Site 2:
HindIII; Ochrobactrum anthropi is an important microbe
having potential for the bioremediation of environments
contaminated by aliphatic compounds. We have constructed
a BAC library for O. anthropi that provides a 90x genome
coverage based on an estimated genome size of 3.83 Mb.
The library contains 3072 clones with an average insert
size of 112 kbp. High-density colony filters of the
library were made and a physical map of the genome
constructed using a hybridization without replacement
strategy. In addition, 624 randomly chosen BAC clones
were HindIII fingerprinted and analyzed using Fingerprint
Contig (FPC; Sangre Centre, UK). The FPC results closely
supported and verified the hybridization contig data.
After determining a reduced tiling path of 69 clones,
138 BAC ends were sequenced for a genome wide survey of
gene distribution and gene structure."

FEATURES
source
1. 577
/organism="Ochrobactrum anthropi"
/mol_type="genomic DNA"
/db_xref="taxon:529"
/clone="3P02-39r"
/lab_host="DH10B E. coli"
/clone_lib="Ochrobactrum anthropi BAC Library"
/note="Vector: pBelosAC11; Site: 1: HindIII; Site 2:
HindIII; Ochrobactrum anthropi is an important microbe
having potential for the bioremediation of environments
contaminated by aliphatic compounds. We have constructed
a BAC library for O. anthropi that provides a 90x genome
coverage based on an estimated genome size of 3.83 Mb.
The library contains 3072 clones with an average insert
size of 112 kbp. High-density colony filters of the
library were made and a physical map of the genome
constructed using a hybridization without replacement
strategy. In addition, 624 randomly chosen BAC clones
were HindIII fingerprinted and analyzed using Fingerprint
Contig (FPC; Sangre Centre, UK). The FPC results closely
supported and verified the hybridization contig data.
After determining a reduced tiling path of 69 clones,
138 BAC ends were sequenced for a genome wide survey of
gene distribution and gene structure."

ORIGIN
Query Match
26.1%; Score 126.4; DB 28; Length 577;

```

[illegible]

RESULT 10	
BF633873/c	
LOCUS	305 bp mRNA linear EST 19-DEC-2000
DEFINITION	NP072A05DT1F1036 Drought Medicago truncatula cDNA clone NF072A05DT
ACCESSION	BF633873
VERSION	BF633873.1
KEYWORDS	5', mRNA sequence.
SOURCE	GI:11898031
ORGANISM	EST
	Medicago truncatula (barrel medic)
	Medicago truncatula
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
	Medicago.
REFERENCE	1 (bases 1 to 305)
AUTHORS	Torrez-Jerez, I., Scott, A. D., Harris, A. R., Gonzales, R. A., Bell, C. J.,
	Flóres, H. R., Imman, J. T., Wellner, J. W. and May, G. D.
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation
JOURNAL	Medicago truncatula drought library
COMMENT	Unpublished (2000)
	Contact: May GD

Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7391  
Fax: 580 221 7380  
Email: gdmay@noble.org  
Insert Length: 305 Std Error: 0.00  
Plate: 072 Row: A Column: 05  
Seq primer: TCACACAGGAACGCTATGAC.  
Location/Qualifiers  
1..305  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"  
/clone="NF072A05DT"  
/tissue\_type="plantlets"

```

/dev_stage="Pooled timepoints"
/clone_lib="Drought"
/notes="Vector: Lambda Zap; Contains a mixture of entire
plantlets harvested in a series of days-post-watering
timepoints. "

ORIGIN

Query Match 25.4%; Score 123; DB 10; Length 305;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 362 GCTGCCATATGGATGGATGTTAACTGTAAGAGCCACTACTACGGAAAACTGGGATTTACCG 421
|||||
Db 305 GCTGCCATATGGATGGATGTTAACTGTAAGAGCCACTACTACGGAAAACTGGGATTTACCG 246
|||||
Qy 422 GACGTGGGGAAGGATTCCTGTGTGAAGCGGTGGCGCTACTCATTAAAGCAACAAAAATGAT 481
|||||
Db 245 GACGTGGGGAAGGATTCCTGTGTGAAGCGGTGGCGCTACTCATTAAAGCAACAAAAATGAT 186
|||||
Qy 482 TGA 484
|||||
Db 185 TGA 183

```

RESULT 11	ACCESSION	ORGANISM
BF634326/c	VERSION	
LOCUS	KEYWORDS	
DEFINITION	SOURCE	

BF634326 305 bp mRNA linear EST 19-DEC-2000  
NF074G12D1F1099 Drought Medicago truncatula cDNA clone NF074G12DT  
5'... mRNA sequence.

BF634326  
BF634326.1 GI:11898484

EST.  
Medicago truncatula (barrel medic)

**Medicago truncatula**

**DISCUSSION**

## REFERENCE

## AUTHORS

TITLE

11

**JOURNAL**

COMMENT

# 100

## FEATURES

Source

## ORIGIN

Query Ma

Best Loc

## Matches

Qy

2.

```

Db      305  GCTGCCATATGATGATGTTAACTGTAAGAGCCACTACTACGAAAAAATCGGATTTACCG 246
|||
Qy      422  GACGTGGGGAAGGATTCCTGTGAAGCGGTGGCGCTACTCATTAAGGCAACAATAATGAT 481
|||
Db      245  GACGTGGGGAAGGATTCCTGTGAAGCGGTGGCGCTACTCATTAAGGCAACAATAATGAT 186
|||
Qy      482  TGA 484
|||
Db      185  TGA 183
|||

RESULT 12
BI873743
LOCUS
DEFINITION
963110H07.y1 C. reinhardtii CC-1690, Stress condition I,
normalized, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA
sequence.
BI873743
BI873743.1 GI:16071747
EST.
SOURCE
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadales; Chlamydomonas.
REFERENCE
1 (bases 1 to 642)
Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C.,
Lefebvre, P., McDermott, J.P., Shreger, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Uncellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 963
Unpublished (2001)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.

FEATURES
source
1..642
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress condition I,
normalized, Lambda Zap II"
/note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP-N (30 min, 1hr, 4hr), TAP-S (30 min,
1hr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NH4 (30min,
1hr, 4hr) and NH4 to NO3 (30min, 1hr, 4hr). PolyA mRNA was
purified from each sample, pooled and cDNA synthesized.
The cDNA was directionally cloned into lambda Zap II
(Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with Exassist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

ORIGIN
Query Match 25.3%; Score 122.4; DB 12; Length 642;
Best Local Similarity 54.0%; Pred No. 6.7e-22;
Matches 249; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

Qy      4 CGAATTGGACACGGTTTTCAGTACATGCCCTTTGGCGGTGAAGGCCCAATATCATTCGTT 63
|||
Db      142  CGCGTTGGGACCGGCTTTGACCTGCAACCGCTGGCGAGGGGTACAACTCATTAATGGC 201
|||

Qy      64  GCGGTACGCATTCCTTACAAAAGGATTGCTGGCGATTCTGATGGCGAGTGGCGGCTC 123
|||
Db      202  GGTATCGACATCCCCCACCAAGGGCTGCGAGGCCCACTCCGATGGCGAGTGTGCTG 261
|||

```

```

Qy      124  CATGCTTACCGATGCATTCCTTGGCGGGCGCGCTGGGGATATCGGAAGCTGTTTC 183
|||
Db      262  CACACCGTGACGAGCGCTATCTCGCGCTGTGTGCTCCAGACATCGCGCAGTGTTC 321
|||
Qy      184  CCGGATACCGATCCCGCATTTAAAGGTGCGATAGCCGGAGCTGCTACGCCGAAGCTGG 243
|||
Db      322  CCAGACACGACCCCAAGTGGAAAGGGCGGCCCTCGACATCTTCTTAAGAGGGGTC 381
|||
Qy      244  CCGTGTATTCAGCGGAAGGGTTATACCTTGGCAACGTGATGTCACTATCATCGTCTAG 303
|||
Db      382  CGGCTGATGGATGAGAAGGGTTACGTGTGGGGAACCTGAGCTGCACCATCATCGCGCAG 441
|||
Qy      304  GCACCGAAGATTTGCCCGCACATTCACAATAGCGCGTGTATTATGCCGAAGATCTCGC 363
|||
Db      442  AAGCCCAAGCTGTGCCCGCACCAAGGAGAACATCCGCAACAACCTGAGTGCCATCTGGGC 501
|||
Qy      364  TGCCATATGGATGATGTTAAAGTGAAGCACTACTACGAAAAAATCGGATTTACCGGA 423
|||
Db      502  GGTGACCCCTCGTTGTCAACATCAAGGCCAAGACGCGAGAGAGGTGATAGCTGNGC 561
|||
Qy      424  CGTGGGAAGGATTCCTGTGAAGCGGTGGCGCTACTCAT 464
|||
Db      562  GAGGAGCGCTCCATCGCTGCCACCGCTGTGTGATGCTTAT 602
|||

RESULT 13
BU238300
LOCUS
DEFINITION
Ds01_15m07 A Ds01 AAPC ECORC cold stressed Flixweed seedlings
Descurainia sophia cDNA clone Ds01_15m07, mRNA sequence.
ACCESSION
BU238300
VERSION
BU238300.1 GI:22750125
KEYWORDS
EST.
SOURCE
Descurainia sophia
Descurainia sophia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Descurainia.
REFERENCE
1 (bases 1 to 773)
Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J.,
Hattori, J.I., Ouellet, T., Robert, L.S., Spratt, D. and Tinker, N.A.
Expressed Sequence Tags from Cold-Stressed Descurainia sophia
Seedlings
Unpublished (2001)
Contact: Singh, J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA
OC6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.
Location/Qualifiers
1..773
/organism="Descurainia sophia"
/mol_type="mRNA"
/db_xref="taxon:89411"
/clone="Ds01_15m07"
/tissue_type="leaf, stem"
/dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
/gs"
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: Eco RI;
Site 2: Xho I; Plants were grown for 1 month at 20oC/16
hrs light/day (average 8 leaves, 1 cm tall, weight
0.02g/plant). Then they were exposed to 2oC, 12 hrs
light/day, for 1 week. Library prepared by C. Piche using
Stratagene kit."

ORIGIN
Query Match 25.0%; Score 121; DB 13; Length 773;
Best Local Similarity 53.5%; Pred. No. 1.7e-21;

```





Box 352145, Seattle, WA 98105-2145, USA  
Tel: 20622216954  
Fax: 2066857244  
Email: [craymond@u.washington.edu](mailto:craymond@u.washington.edu)  
Class: [shotgun](#).

```

FEATURES
source
1. .811
location/Qualifiers
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="MSH"
/db_xref="taxon:287"
/clone_lib="msl2_5245"
/note="Environmental isolate. Whole
library."

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## ORIGIN

Query Match	24.6%	Score 119;	DB 28;	Length 811;
Best Local Similarity	59.7%	Pred. No. 5.9e-21;		
Matches 200;	Conservative 0;	Mismatches 135;	Indels 0;	Gaps 0;
QY	1	ATCGGAATTGACACGGTTTTTGAGTACATCGCCTTTGGCGGTGAAGCCCAATATCATTT	60	
Db	441	ATCGGAATTGGCCATGGCTACGAGTGCATCGCTTCGGCGAGGCGGACTTCATCACCTC	500	
QY	61	GGTGGCGCTACGCAATTCCTTACGAAAAAGGATTGCTGGCGCAATTCGTATGGCGAGCTGGCG	120	
Db	501	GGCGGCGTGGCAATTCCTCCCAACATATGGGCTGGTCGGCCACTCCGACGGCGAGCTGCTG	560	
QY	121	CTCCATCGCTTGACCGATGCAATTCCTTTGGCGCGCGCGGCTTGGGGGATATCGGCAAGCTG	180	
Db	561	CTGCACGCCCTTGTCCGATGCGCTCTCAGCGCGCGCGCTCTTGGCGGACATTCGCAAGCAA	620	
QY	181	TTCCGGATACCGATCCGGCAATTTAAAGGTGCCGATAGCCGCGAGCTGTACGGGAGCC	240	
Db	621	CTTCGGACACCGACCCGGGGTTCAGGGGCGCTTCAGAGTTCGACGCTTCCTGCGACACGTG	680	
QY	241	TGCGCTCGTATTGAGGGCGAAGGGTTATACCCCTTGGCAACGTCGATGTCATTCATCGCT	300	
Db	681	TGCTCAATCGTGGCGATAAGGGCTGTAAAGTCGTACATTTTTCGCCCATTTGTCATCC	740	
QY	301	CAGGACCGAAGATGTTGGCGCACATTCACAAAT	335	
Db	741	AATCGTTTCGAAATTTGGTCGGAATTCGAGACCAAT	775	

Search completed: June 16, 2004, 06:30:13  
Job time : 2152.75 secs

